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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:18:03 ; Search time 1460.69 Seconds
(without alignment)
12007.805 Million cell updates/sec

Title: US-09-807-933B-6

Perfect score: 1083
Sequence: 1 atgaagttccctaccattgc.....ctgctcgtccaagaataa 1083

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estinu:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrc:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rnd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	179	16.5	691	10 BE585661 EST#6PSP6
2	146.2	13.5	450	13 BI2007229
3	128.6	11.9	444	13 BI190695
4	122.2	11.3	426	13 BI187295
5	86	7.9	215	13 BI190568
6	85.6	7.9	619	17 FR0047601

C	7	84	7.8	989	17	CNS02HNA4	AL197365 Tetradon
C	8	81.6	7.5	735	17	CNS04NSM	AL229119 Tetradon
9	78.8	7.3	331	17	BH881398	BH881398 hv25c11.b	
10	78.8	7.3	933	17	AZ204694	SP 0100_A	
11	77.8	7.2	350	17	BH879665	BH879665 hc47h12.g	
12	77.8	7.2	788	17	AZ183942	SP 1002_A	
13	77.8	7.2	914	17	AZ205202	SP 0100_A	
14	77.6	7.2	494	17	FR0048073	AL444858 Fugu rubr	
15	76.4	7.1	259	13	BI187393	BI187393 a3b03fs.r	
16	76.2	7.0	250	13	BH878991	h858e08.b	
17	75.4	7.0	289	13	BI191461	BI191461 K3g10fs.r	
C	18	75.2	6.9	627	17	BH179321	BH179321 014_P_01-
C	19	75.2	6.9	627	17	CNS07LFL	AL616275 T7 end of
C	20	75.2	6.9	824	17	AZ185454	SP 1005_A
21	74	6.8	500	17	B67199	B67199 CPG0015B Cp	
C	22	73	6.7	454	17	AZ178507	SP 0161_B
23	73	6.7	501	17	FR0048173	AL444958 Fugu rubr	
24	72.8	6.7	522	13	BI783235	BI783235 K48909.Y	
25	72.4	6.7	450	17	FR0025683	AL018519 F. rubripe	
26	72.4	6.7	621	17	AZ164800	SP 0076_B	
27	71.8	6.6	335	10	AM275677	xp08e07.x	
28	71.2	6.6	274	13	BI188678	BI188678 d2c10fs.r	
29	71.2	6.6	280	13	BI190362	BI190362 h4h07fs.r	
30	71.2	6.6	289	13	BI189728	BI189728 g1c06fs.r	
C	31	70.8	6.5	230	17	BH869848	hms4h10.g
C	32	70.8	6.5	530	17	AZ166409	SP 0088_A
C	33	70.4	6.5	810	17	AZ199472	SP 1039_B
34	69.8	6.4	533	9	AA495649	c073_zho1	
35	68.8	6.4	358	17	BH777606	BH777606 f2mb013f0	
36	68.4	6.3	278	17	BH871622	BH871622 h35f05.b	
37	68.4	6.3	834	17	AZ188004	SP 1011_A	
38	67.8	6.3	273	17	FR0047466	AL444251 Fugu rubr	
39	66	6.1	475	17	AZ145091	SP 0044_A	
40	66	6.1	790	17	CNS0379X	AZ145091 SP 0044_A	
41	65.8	6.1	793	17	CNS01VTG	AL169549 Tetradon	
42	64.8	6.0	774	17	BH355163	BH355163 CH230-81P	
43	64.6	6.0	619	17	FR0047503	AL444288 Fugu rubr	
44	64.4	5.9	796	17	AZ186967	SP 1008_A	
45	64	5.9	977	17	CNS0678C	AL414226 T7 end of	

ALIGNMENTS

RESULT 1
LOCUS BE585661 691 bp mRNA linear EST 17-AUG-2000
DEFINITION EST#6PSP6_D02_d2_014 KSU wheat Fusarium graminearum infected spike
CDNA library Trilicium aestivum CDNA clone EST#6PSP6_D02_d2_014,
mRNA sequence.

ACCESSION BE585661
VERSION BE585661.1 GI:9838604

KEYWORDS
SOURCE EST.

ORGANISM bread wheat.

REFERENCE
AUTHORS Fellers,D.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.
TITLE The structure and function of the expressed portion of the wheat
genomes - Kansas State University, Fusarium graminearum infected
spike CDNA library

JOURNAL COMMENT
Unpublished (2000)
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
Email: jpf@alfalfa.ksu.edu

Sequence have been trimmed to remove vector sequence and low

quality sequence with phred score less than 20
Seq primer: SP6.

FEATURES
Location/Qualifiers
source

1..691
/organism="Triticum aestivum"
/cultivar="Sumai3"
/db_xref="taxon:4565"
/clone="EST#6PSP6 D02 d2 014"
/clone_lib="KSU wheat Fusarium graminearum infected spike
cDNA library"
/issue_type="spike"
/dev_stage="Adult Plant"
/lab_host="E. coli JM109"
/note="Vector: pGEM-T easy; Site 1: SacI; Site 2: SpeI;
plants were grown in the greenhouse. Spikes were sprayed
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. cDNA was
prepared using the SmartTM PCR cDNA synthesis kit from
Clontech. cDNA was cloned into the pGEM-T easy vector
from Promega."

BASE COUNT 135 a 196 c 163 g 197 t

Query Match 16.5%; Score 179; DB 10; Length 691;
Best Local Similarity 65.5%; Pred. No. 5.7e-36;
Matches 298; Conservative 0; Mismatches 145; Indels 12; Gaps 2;

449 GTGTGCTCCCGGATATGTGAACCACTGCTACTAGGATTTGTGTAAGCTTTTGA 508
160 GTGTGCTCTTCTGGAAGTGTCACTGATCTGAGTCTGCAAGCTTTCTTGT 219
509 GTTGGCCCGGTAAAGCTGATGTCACTCCCTGTTGGCTCTGTAAAGATGTAGA 568
220 CTGGAGATGGCAAGCCAAAGTCTGCGCCCTGCTTGACTTGTGACAAAAGACAAC 279
569 CTCTTGCATACAACTCAAAACGCGTGTG---TTGGTGTAGACAGTACACTGT 625
280 CCACTACTACCTGAACCCCTCAACGGTTGTGAGATGGTGTGCTTTGCTTGTGA 339
626 ATGACATCAACTTTGGTGTGACGACACCTTGGCTTGGCTTGGCGCTTCCA 685
340 CTAATCTACCTCCCTGGGCTGTCAACGACCTTGTGAGGTTTACTGCTACCAAG 399
686 TTTCTGTGTGTAAGCACTACTGTTGCTGCTTTGCACTCACTCACTCTTA 745
400 TTGCTGTGTGCACTGACACAGCTGTGTCTGTGTATGCTCTTACGACG 459
746 CTGCGGTCAAGGGTAAGATGTTGTCAAGTACCACTGTTGACCTTGGCT 805
460 GTCCCGTAAAGGAAAGATGATGTCAGTCCACCACTGTTGTGTATCTCGGTG 519
806 CTAACTGCTGTCTACTTTGACTTGAAGTCCGCGTGTGTGTGTGTATCTACA 865
520 ATAAAC-----CACTTGAACCTTATGATCCCGGCGGTGTGTGTATTCATG 570
866 GTGTGCTCACTCAATGCGGTGTCTCCACCGATGT 900
571 GATGCACTCTGATGTTCCGCAAGCCCTGTGTGT 605

RESULT 2
BI200729 450 bp mRNA linear EST 10-JUL-2001
LOCUS BI200729
DEFINITION library Fusarium sporotrichioides cDNA clone o1f05t5 5', mRNA

ACCESSION BI200729
VERSION BI200729.1 GI:14666701
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium.

REFERENCE 1 (bases 1 to 450)
Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand

TITLE
JOURNAL
COMMENT
Analysts of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
633 5e-66 g11170140|sp|P45699 POTATIVE ENDONUCLEASE TYPE
KPRCUNSOR (EN
Seq primer: T3
High quality sequence stop: 440.

FEATURES
Location/Qualifiers
source

1..450
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 90 a 125 c 102 g 133 t

Query Match 13.5%; Score 146.2; DB 13; Length 450;
Best Local Similarity 67.6%; Pred. No. 1.8e-27;
Matches 221; Conservative 0; Mismatches 103; Indels 3; Gaps 1;

449 GTGTGCTCCCGGATATGTGAACCACTGCTACTAGGATTTGTGTAAGCTTTTGA 508
124 GTGTGCTCTTCTGGAAGTGTCACTGATCTGAGTCTGCAAGCTTTCTTGT 183
509 GTTGGCCCGGTAAAGCTGATGTCACTCCCTGTTGGCTCTGTAAAGATGTAGA 568
184 CTGGAGATGGCAAGCCAAAGTCTGCGCCCTGCTTGACTTGTGACAAAAGACAAC 243
569 CTCTTGCATACAACTCAAAACGCGTGTG---GTTGTGTAGACAGTACACTGT 625
244 CCACTACTACCTGAACCCCTCAACGGTTGTGAGATGGTGTGCTTATGCTTGA 303
626 ATGACATCAACTTTGGTGTGACGACACCTTGGCTTGGCTTGGCGCTTCCA 685
304 CCACTACTCCCGGCTGTCAACGACCTTGTGAGGTTTGTGCTGCTACCAAG 363
686 TTTCTGTGTGTAAGCACTACTGTTGCTGCTTTGCACTCACTCACTCTTA 745
364 TTGCTGTGTGTAAGCACTACTGTTGCTGCTTTGCACTCACTCACTCTTA 423
746 CTGCGGTCAAGGGTAAGATGTTG 772
424 GTCCCGTAAAGGCAAGATGATG 450

RESULT 3
BI190695 444 bp mRNA linear EST 10-JUL-2001
LOCUS BI190695
DEFINITION library Fusarium sporotrichioides cDNA clone 13g10f5 5', mRNA

ACCESSION BI190695
VERSION BI190695.1 GI:14664374
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

REFERENCE 1 (bases 1 to 444)
 AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)
 COMMENT Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 576 3e-59 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KRECURSOR (EN)
 Seq primer: T3.
 Location/Qualifiers
 1..444
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="1391018"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 85 a 127 c 92 g 140 t
 ORIGIN

Query Match 11.9%; Score 128.6; DB 13; Length 444;
 Best Local Similarity 67.1%; Pred. No. 7.1e-23;
 Matches 198; Conservative 0; Mismatches 94; Indels 3; Gaps 1;

449 GTGTGCTCCGGTAAAGTGAACCACTGCTAATGGATGTTGAAGCTTCTTGA 508
 150 GTGTGCTTCTGGAAGTGGCACTCTAATGATGGAAGCTGCAAGCTTCTTGT 209
 509 GTTGACCGGTGAAGCTGATGTCACCTCCCTGTTGCTCTGTAACAAGATGTAGA 568
 210 CTGGAGGCGCAAGGCTAAAGTCAAGCGCCCTGCTGCTGATGTAACAAGAATAACC 269
 569 CTCTTGCGATTAACAACACTGAACGCGCTGTTGTTGTTGATGACGCTTGA 625
 270 CTATCACTAACCTGAACGCTGTCACGCTGTTGAGGTTGCTGCTTAATGCTTGA 329
 626 ATGACAATCAACTTGGGTTGTTAGCGACGACCTTGCCTAAGTTGCGCGCTTCCA 685
 330 CCAACTACTCCCGTGGGCTGTCAACGACGACCTTGTACGGTTTCCGTCTACCAAGC 389
 686 TTTCTGTTGTTAGCGAAGCTACTTGGTGTGCTGCTTTGCAATCAATTCAC 740
 290 TTGCTGGTGTAGTAGAGCCAGCTGTGCTGTGCTTAATGCTCACTTTCAC 444

RESULT 4
 B1187295 426 bp mRNA linear EST 10-JUL-2001
 LOCUS alh1lf1.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 DEFINITION library Fusarium sporotrichioides cDNA clone alh1lf 5', mRNA
 sequence.
 ACCESSION B1187295
 VERSION B1187295.1 GI:14660974
 SOURCE EST.
 ORGANISM Fusarium sporotrichioides.
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; microsporitic Hypocreales; Fusarium.
 REFERENCE 1 (bases 1 to 426)
 AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)

TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)
 COMMENT Other ESTs: alh1lf.f1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability. Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 565 5e-58 g|1170140|sp|P45699 PUTATIVE ENDOGLUCANASE TYPE
 KRECURSOR (EN)
 Seq primer: T3
 High quality sequence stop: 338.
 Location/Qualifiers
 1..426
 /organism="Fusarium sporotrichioides"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="alh1lf1"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 82 a 119 c 91 g 134 t
 ORIGIN

Query Match 11.3%; Score 122.2; DB 13; Length 426;
 Best Local Similarity 66.6%; Pred. No. 3.3e-21;
 Matches 191; Conservative 0; Mismatches 93; Indels -3; Gaps 1;

449 GTGTGCTCCGGTAAAGTGAACCACTGCTAATGGATGTTGAAGCTTCTTGA 508
 140 GTGTGCTTCTGGAAGTGGCACTCTAATGATGGAAGCTGCAAGCTTCTTGT 199
 509 GTTGACCGGTGAAGCTGATGTCACCTCCCTGTTGCTCTGTAACAAGATGTAGA 568
 200 CTGGAGGCGCAAGGCTAAAGTCAAGCGCCCTGCTGCTGATGTAACAAGAATAACC 259
 569 CTCTTGCGATTAACAACACTGAACGCGCTGTTGTTGTTGATGACGCTTGA 625
 260 CTATCACTAACCTGAACGCTGTCACGCTGTTGAGGTTGCTGCTTAATGCTTGA 319
 626 ATGACAATCAACTTGGGTTGTTAGCGACGACCTTGCCTAAGTTGCGCGCTTCCA 685
 320 CCAACTACTCCCGTGGGCTGTCAACGACGACCTTGTACGGTTTCCGTCTACCAAGC 379
 686 TTTCTGTTGTTAGCGAAGCTACTTGGTGTGCTGCTTTGCAATTCAC 732
 380 TTGCTGGTGTAGTAGAGCCAGCTGTGCTGTGCTTAATGCTCACTTTCAC 426

RESULT 5
 B1190568 215 bp mRNA linear EST 10-JUL-2001
 LOCUS l2e1lf1.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 DEFINITION library Fusarium sporotrichioides cDNA clone l2e1lf 5', mRNA
 sequence.
 ACCESSION B1190568
 VERSION B1190568.1 GI:14664247
 SOURCE EST.
 ORGANISM Fusarium sporotrichioides.
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreales; microsporitic Hypocreales; Fusarium.
 REFERENCE 1 (bases 1 to 215)
 AUTHORS Ren, Q., Tag, A., Peplow, A., Lai, H., Kupfer, C., Peterson, A., Beremand
 TITLE Analysis of a Fusarium sporotrichioides EST database
 JOURNAL Unpublished (2001)

COMMENT

Other ESTs: i2ellfs.f1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry, University of Oklahoma
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability included
 is the best homolog from a black search of Genbank nr 04-09-01
 363 7e-35 g11170140|sp|P45699. PUTATIVE ENDOGLUCANASE TYPE
 KPCURSOR (EN
 Seq primer: T3
 High quality sequence stop: 156.

FEATURES

source

Location/Qualifiers
 1. 215
 /organism="Fusarium sporotrichioides"
 /strain="T1 10"
 /db_xref="taxon:5514"
 /clone="i2ellfs"
 /clone_lib="Fusarium sporotrichioides T1 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into XhoI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"
 44 a 61 c 53 g 56 t 1 others

BASE COUNT

ORIGIN
 Query Match 7.9%; Score 86; DB 13; Length 215;
 Best Local Similarity 65.6%; Pred. No. 6.9e-12;
 Matches 141; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

481 TACTGGATTGTTGTTGACCTTCTTGTGACGTTGCGCCGTTAGGCTGATGCACTCCCTC 540
 1 TACTGGACTGTGACGCTTCTTGTGACGCGCAAGCTAAAGTCAGCGCCCT 60
 541 GTTGCTCTGTGAACAGAGTGTAGACTCTGTGATAACAACACTCAAAACGCGTGT 600
 61 GCTGTGACTTGTGACAAAGATTAACCTTACTACTAAGCGTGTGCAAGCGTGT 120
 601 ---GTTGTGTAGAGGCTGACCTGTATGACCAACTCACTTGGTTGTAGGAGAGAC 657
 121 GAGGTTGTGTGCTTGTGCTATGCTGACCAACTCTCCCGTGGCTGTCAAGAGAC 180
 658 CTTCCTACGCTTTCGCCGCTGCTCCATTCTGG 692
 181 CTGCTTACGCTTTCGCTGCTACCAACTTGTCTGG 215

RESULT 6
 PR0047601 619 bp DNA linear GSS 05-JAN-2001

LOCUS
 Pugu rubripes GSS sequence, clone 217A13J11, genomic survey

DEFINITION
 sequence.
 AL444386 GI:12052222

ACCESSION
 AL444386.1 GI:12052222

VERSION
 GSS: genome survey sequence.

KEYWORDS
 Takifugu rubripes.

SOURCE
 ORGANISM

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT
 V type: pBluescript II KS
 PRIMER: KS
 DESCR:

FEATURES

source

Location/Qualifiers
 1. 619
 /organism="Takifugu rubripes"
 /db_xref="taxon:3103"
 /clone="217A13J11"
 /clone_lib="BAC 217A13"
 102 a 172 c 92 g 177 t 76 others

BASE COUNT

ORIGIN
 Query Match 7.9%; Score 85.6; DB 17; Length 619;
 Best Local Similarity 48.3%; Pred. No. 1.6e-11;
 Matches 190; Conservative 0; Mismatches 203; Indels 0; Gaps 0;

193 AATGAAACCTCAGCTCCATCAACAAATCTTTCACAAACACCACTACTGAGAGTGC 252
 7 ACTGACAGCATCTACTACTGATGATGATGATGATGATGATGATGATGATGATGAT 66
 253 AAGAGACTACCACTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 312
 67 ACTGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 126
 313 ACCACACTACTGAGGCTTCCAGAGACCACTACTGAGGCTTGAAGACACAC 372
 127 GCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 186
 373 ACTACTACTAGAGGCTTCTACTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 432
 187 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 246
 433 TACTCCGCT 492
 247 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 306
 493 TGTAGGCTTCTGCAAGTGGCCGAGTGAAGCTGATGATGATGATGATGATGATGATG 552
 307 ACTACTCTGATCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 366
 553 AACAGAGTGTAGACTCTTGTGATTAACAC 585
 367 ACTAGCTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 399

RESULT 7
 CNS02HA4 989 bp DNA linear GSS 13-MAY-2000

LOCUS
 Tetraodon nigroviridis genome survey sequence T7 end of clone
 139021 of library G from Tetraodon nigroviridis, genomic survey

DEFINITION
 sequence.
 AL197365 GI:7835515

ACCESSION
 AL197365.1 GI:7835515

VERSION
 GSS: genome survey sequence.

KEYWORDS
 Tetraodon nigroviridis.

SOURCE
 ORGANISM

REFERENCE
 AUTHORS

TITLE
 JOURNAL

COMMENT
 V type: pBluescript II KS
 PRIMER: KS
 DESCR:

One pass dye-terminator sequencing of BAC (pBelOBAC11) cloned
 genomic sequence
 The BACs can be obtained from <http://www.incyte.com>.
 Location/Qualifiers
 1. 619
 /organism="Takifugu rubripes"
 /db_xref="taxon:3103"
 /clone="217A13J11"
 /clone_lib="BAC 217A13"
 102 a 172 c 92 g 177 t 76 others

JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 989)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000)
 COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
 source
 1. 989
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone="139021"
 /clone_lib="G"
 /note="Genoscope sequence ID : COAG139AH1LP1-end : T7"

BASE COUNT 320 a 245 c 122 g 261 t 41 others

ORIGIN

Query Match 7.8%; Score 84; DB 17; Length 989;
 Best Local Similarity 50.3%; Pred. No. 5.3e-11;
 Matches 190; Conservative 3; Mismatches 185; Indels 0; Gaps 0;

QY 209 CCACTAACAAATCTTCTCAGAAAACCACTAGAGTGCAGAGAGCTACCACTA 268
 |||||
 DB 157 CTACTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 216
 |||||

QY 269 CTAAAGGTTCCAGAAAGACCACTAGAGTGCAGAGAGCTACCACTA 328
 |||||
 DB 217 CTACTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 276
 |||||

QY 329 CTTCAGAGAGAGACCACTAGAGTGCAGAGAGCTACCACTA 388
 |||||
 DB 277 CTACTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 336
 |||||

QY 389 CTTCACCTGCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 448
 |||||
 DB 337 CTACTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 396
 |||||

QY 449 GTGGTCCCTCCGGAATGAGTGAACCACTGCGTACGAGTGTGTAAGCTCTTGA 508
 |||||
 DB 397 CTACTACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 456
 |||||

QY 509 GTTGGCCCGGTAAGGCTGATGACCTCCCTGTTGGCTCTTAACAAGAGTGTAGA 568
 |||||
 DB 457 NTNGTNGTGGTGGGAGTGTGCTCTACTACTACTACTACTACTACTACTACTA 516
 |||||

QY 569 CTCTTGCTGATTAACACA 586
 |||||
 DB 517 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 534
 |||||

RESULT 8
 CNS04NSM 735 bp DNA linear GSS 21-MAY-2000
 LOCUS Tetraodon nigroviridis genome survey sequence T7 end of clone
 DEFINITION 123M05 of library G from Tetraodon nigroviridis, genomic survey
 sequence.
 ACCESSION AL299119
 VERSION AL299119.1 GI:8038260
 KEYWORDS GSS: genome survey sequence.
 SOURCE Tetraodon nigroviridis.
 ORGANISM Tetraodon nigroviridis.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Tetraodontiformes; Tetraodontidae; Tetraodon.
 1 (bases 1 to 735)

REFERENCE
 AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Bouneau,L., Fisher,C.,
 Bernot,A., Fitzames,C., Wincker,P., Brothier,P., Quetier,F.,
 Saurin,W. and Weissenbach,J.
 Human gene number estimate provided by genome wide analysis using
 Tetraodon nigroviridis DNA sequence

JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 735)
 AUTHORS Roest-Crollius,H., Jallion,O., Dasilva,C., Fitzames,C., Fisher,C.,
 Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
 Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the
 freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 735)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000)
 COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.

FEATURES
 source
 1. 735
 /organism="Tetraodon nigroviridis"
 /db_xref="taxon:99883"
 /clone="123M05"
 /clone_lib="G"
 /note="Genoscope sequence ID : COBG123AC03LP1-end : T7"

BASE COUNT 242 a 45 c 223 g 197 t 28 others

ORIGIN

Query Match 7.5%; Score 81.6; DB 17; Length 735;
 Best Local Similarity 59.0%; Pred. No. 1.9e-10;
 Matches 138; Conservative 1; Mismatches 95; Indels 0; Gaps 0;

QY 205 ACCCTCACTAACAAATCTTCTCAGAAAACCACTAGAGTGCAGAGAGCTACCACTA 264
 |||||
 DB 319 ACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 260
 |||||

QY 265 ACTACTAAGGTTCCAGAAAGACCACTAGAGTGCAGAGAGCTACCACTA 324
 |||||
 DB 259 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 200
 |||||

QY 325 GAAGCTTCCAGAAAGACCACTAGAGTGCAGAGAGCTACCACTA 384
 |||||
 DB 199 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 140
 |||||

QY 385 AAGGCTTCACTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 438
 |||||
 DB 139 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 86
 |||||

RESULT 9
 BH881398 331 bp DNA linear GSS 05-AUG-2002
 LOCUS hv25c11.b1 WGS-Zmay9f (JM107 adapted methyl filtered) Zea mays
 DEFINITION genomic clone hv25c11 5', DNA sequence.
 ACCESSION BH881398
 VERSION BH881398.1 GI:22117295
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 331)

REFERENCE
 AUTHORS Rabinowicz,P.D., O'Shaughnessy,A.L., Ballia,V., Dedhia,N.,
 Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
 Zuberavert,I., McCombie,W.R. and Martienssen,K.A.
 Genomic shotgun sequences from Zea mays (methyl-filtered)
 Unpublished (2002)
 CONTACT: W. Richard McCombie
 Iltis Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel.: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org

Plate: hv25 row: c column: 11
 Seq primer: -21M3UnivFwd
 Class: Shotgun
 High quality sequence stop: 331.
 Location/Qualifiers

FEATURES

source

1..331
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="hv25c11"
 /lab_host="JM107 or DH5a"
 /note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector l.x/y reads in M13mp19. b/g reads in pUC19. The same ligation was transformed in either JM107 or DH5a."
 BASE COUNT
 110 a 108 c 6 g 107 t
 ORIGIN

Query Match
 Best Local Similarity 58.5%; Pred. No. 6,7e-10;
 Matches 137; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 205 ACCTCCTACCAATCTTCTCACAACCAACCACTGAGAGTCCAGAGAACTAC 264
 DB 15 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 74
 QY 265 ACTACTAAGGTTCCAGAGAACCACTACTGAGAGTCCAGAGAACTACTACT 324
 DB 75 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 134
 QY 325 GAAGCTCCAGAGAACCACTACTGAGAGTCCAGAGAACTACTACTACTACTACT 384
 DB 135 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 194
 QY 385 AAGGCTTACTACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 438
 DB 195 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 248

RESULT 10
 AZ204694 933 bp DNA linear GSS 31-AUG-2000
 LOCUS SP 0100_A1 G12 SP66 Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus
 DEFINITION genomic clone Plate=100 Col=23 Row=M, DNA sequence.
 ACCESSION AZ204694.1 GI:8399614
 VERSION AZ204694.1
 KEYWORDS GSS.
 SOURCE Strongylocentrotus purpuratus.
 ORGANISM Strongylocentrotus purpuratus
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa; Echinoidea; Echinoidea; Echinacea; Echinoidae;
 Strongylocentrotidae; Strongylocentrotus.
 1 (bases 1 to 933)

REFERENCE

AUTHORS

TITLE

A sea urchin genome project: Sequence scan, virtual map, and additional resources
 JOURNAL MEDLINE
 COMMENT
 Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
 Contact: Cameron, RA, Davidson, EH, Hood, L
 Division of Biology 156-29
 California Institute of Technology
 Pasadena California 91125, USA
 Tel: (626) 395-8421
 Fax: (626) 793-3047

Email: acameron@caltech.edu
 Plate: 100 row: M column: 23
 Seq primer: SP6
 Class: BAC ends
 High quality sequence stop: 933.
 Location/Qualifiers

FEATURES

source

1..933
 /organism="Strongylocentrotus purpuratus"
 /db_xref="taxon:7668"
 /clone="Plate=100 Col=23 Row=M"
 /clone.lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
 /note="Organ: sperm; Vector: BAC63.6; BAC Clones in E-Coli DH10B"
 BASE COUNT
 226 a 235 c 156 g 316 t
 ORIGIN

Query Match
 Best Local Similarity 57.9%; Pred. No. 1.2e-09;
 Matches 140; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 189 TCCCATGAAACCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 248
 DB 209 TACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 268
 QY 249 TGGCAAGAGACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 308
 DB 269 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 328
 QY 309 GAAGACCACTACTGAGAGTCCAGAGAACCACTACTGAGAGTCCAGAGAAC 368
 DB 329 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 388
 QY 369 CACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 428
 DB 389 TACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 448
 QY 429 AA 430
 DB 449 TA 450

RESULT 11
 BH879665 350 bp DNA linear GSS 05-AUG-2002
 LOCUS ht47h12.g1 WGS-ZmayrF (JM107 adapted methyl filtered) Zea mays
 DEFINITION genomic clone ht47h12 5', DNA sequence.
 ACCESSION BH879665.1 GI:22115562
 VERSION BH879665.1
 KEYWORDS GSS.
 SOURCE Zea mays.
 ORGANISM Zea mays.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 350)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA
 Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: ht47 row: h column: 12
 Seq primer: -21M3UnivFwd
 Class: Shotgun
 High quality sequence stop: 350.
 Location/Qualifiers

source

1. .350
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ht47h12"
/lab_host="JM107 or DH5a"
/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in pUC19). The same ligation was transformed in either JM107 or DH5a."

BASE COUNT 112 a 110 c 13 g 115 t

ORIGIN

Query Match 7.2%; Score 77.8; DB 17; Length 350;
Best Local Similarity 55.3%; Pred. No. 1.3e-09;
Matches 151; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

QY 205 ACCTCCACTAACAAATCTTCTACAAACCACTAGAGTCCAGAGACTACC 264
DB 73 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 132
QY 265 ACTACTAAAGTTCCAGAGACCACTACTAGAGCTTAAGAGACCACTACT 324
DB 133 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 192
QY 325 GAAGCTTCCAGAGACCACTACTAGAGCTTAAGAGACCACTACTACTACT 384
DB 193 GCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 252
QY 385 AAGGCTTCACTACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCA 444
DB 253 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 312
QY 445 TCTGTGTGCTCCGGTAATGCGAACCCT 477
DB 313 ACGGCTACTGCTACTAGTACTAGTACTACT 345

RESULT 12
AZ183942 788 bp DNA linear GSS 30-AUG-2000
LOCUS
DEFINITION SP.1002_A1_H11.SP6 Strongylocentrotus purpuratus, purple sea urchin
clone genomic BAC library Strongylocentrotus purpuratus genomic
clone Plate=1002 Col=21 Row=O, DNA sequence.
AZ183942
ACCESSION AZ183942.1 GI:8356317
VERSION
KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus.
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 788)
AUTHORS Cameron,R.A., Mahaitas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
MEDLINE 20402566
COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu

Plate: 1002 row: 0 column: 21
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 788.
Location/Qualifiers

FEATURES
source

1. .788
/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="plate=1002 Col=21 Row=O"
/note="Organ: sperm; Vector: BACs 3.6; BAC clones in E-Coli DH10B"

BASE COUNT 248 a 183 c 98 g 259 t

ORIGIN

Query Match 7.2%; Score 77.8; DB 17; Length 788;
Best Local Similarity 60.8%; Pred. No. 2e-09;
Matches 127; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 221 CTTCTACAAACACCACTAGAGTCCAGAGACTACACTAAAGTTCCA 280
DB 325 CTTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 384
QY 281 AGAAGACCACTACTAGAGCTCTAAGAGACCACTACTAGAGCTTCCAGAGA 340
DB 385 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 444
QY 341 CCACCACTACTAGAGCTCTAAGAGACCACTACTACTAGAGCTTCTACTCTCA 400
DB 445 CCACCACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 504
QY 401 CTTCA 429
DB 505 TTCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 533

RESULT 13
AZ205202 914 bp DNA linear GSS 31-AUG-2000
LOCUS
DEFINITION SP.0100_A2_G12.SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=100 Col=24 Row=W, DNA sequence.
AZ205202
ACCESSION AZ205202.1 GI:8400122
VERSION
KEYWORDS GSS.
SOURCE Strongylocentrotus purpuratus.
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Echinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 914)
AUTHORS Cameron,R.A., Mahaitas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J., Davidson,E.H. and Hood,L.
TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
MEDLINE 20402566
COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
Plate: 100 row: M column: 24
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 914.
Location/Qualifiers
1. .914

Wed Jun 18 17:56:02 2003

us-09-807-933b-6.rst

Page 8

/organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="Plate=100 Col=24 Row=M"
/clone_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: Sperm; Vector: BACs 6, BAC clones in E-Coli DH10B"

BASE COUNT 210 a 208 c 107 g 387 t 2 others

ORIGIN

Query Match
Best Local Similarity 7.2%; Score 77.8; DB 17; Length 914;
Matches 157; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

QY 205 ACCCTCAACAAATCTTCTCCAAACCAACCACTAGAGTGCAGAAAGCTAC 264
DB 202 ACTACTCTACCACTACTACTATTACTACCAACCACTACTACTGCACTACTACT 261
QY 265 ACTACTAAAGGTCAGAGACCACTACTAGAGTGCAGAAAGCTACTACTACT 261
DB 262 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 321
QY 325 GAAGCTCCAGAGACCACTACTAGAGTGCAGAAAGCTACTACTACTACTACT 321
DB 322 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 384
QY 385 AAGGCTCTACCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 381
DB 382 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 444
QY 445 TCTGTGTGTCCTCCGCTGATGAGTGAACCACTGCTGCTGCTGCTGCTGCT 493
DB 442 ACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 490

RESULT 14
FR0048073 494 bp DNA linear GSS 05-JAN-2001
LOCUS Fugu rubripes GSS sequence, clone 263K15Bd8, genomic survey
DEFINITION
ACCESSION AL444858
VERSION AL444858.1 GI:12052694
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes.
ORGANISM Takifugu rubripes.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
Tetraodontidae; Takifugu.
1 (bases 1 to 494)
Clark, M.S.
Direct Submission
Submitted (29-SEP-2000) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB, UK Email:
biohelp@hmp.mrc.ac.uk
Vector: pBluescript II KS
V-type: phagemid
PRIMER: KS
DESCR:
One pass dye-terminator sequencing of BAC (pBelobACII) cloned
genomic sequence
The BACs can be obtained from <http://www.incyte.com>.

FEATURES
source
1..494
Location/Qualifiers
/organism="Takifugu rubripes"
/db_xref="taxon:31033"
/clone="263K15Bd8"
/clone_lib="BAC 263K15"

BASE COUNT 128 a 163 c 45 g 158 t

Query Match
Best Local Similarity 7.2%; Score 77.6; DB 17; Length 494;
Matches 51.1%; Pred. No. 1.7e-09;

Matches 182; Conservative 0; Mismatches 174; Indels 0; Gaps 0;
QY 233 CCACCACTACGAGAGGCGCAAGAAAGTACCTACTTAAGGTCAGAAAGCAACA 292
DB 124 CTACTACTCTACTACTACTAGAGAGAGTGTACTACTACTACTACTACTACT 183
QY 293 CTACTGAGGCTCTAAGAGAGCAACCACTACTAGAGTGTCAAGAGCAACCACT 352
DB 184 CTACTAGGCTGTACTACTACTACTACTACTACTACTACTACTACTACTACT 243
QY 353 AAGCTCTAAGAGAGCAACCACTACTACTAGAGTGTCAAGAGCAACCACT 412
DB 244 CTACTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 303
QY 413 CTCTTGTCTCTCAACCACTACTACTACTACTACTACTACTACTACTACTACT 472
DB 304 CTGCTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 363
QY 473 CCAGTCTACTAGAGATGTTGTTGAGCTCTTGTGAGTGGCCGTAAGAGTGA 532
DB 364 CTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 423
QY 533 CTCTGCTGTGTGCTGCTGTAACAGAGATGTAAGCTTGTGTATTAACAAC 588
DB 424 CTACTGCTGTACTACTACTACTACTACTACTACTACTACTACTACTACTACT 479

RESULT 15
B1187393 299 bp mRNA linear EST 10-JUN-2001
LOCUS B1187393
DEFINITION B1187393.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
sequence.
ACCESSION B1187393
VERSION B1187393.1 GI:14661072
KEYWORDS EST.
SOURCE Fusarium sporotrichioides.
ORGANISM Fusarium sporotrichioides.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; microsporitic Hypocreales; Fusarium.
1 (bases 1 to 299)
Ren, Q., Tag A., Pehlou, A., Lai, H., Kuyfer, C., Peterson, A., Beremand
M., and Roe, S.
Analysis of a Fusarium sporotrichioides EST database
Unpublished (2001)
Contact: Bruce A. Roe, University of Oklahoma, broeseu.edu
Department of Chemistry and Biochemistry
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broeseu.edu
Contact: Dr. Marian Beremand regarding clone availability. Included
is the best homolog from a blastx search of Genbank nr 04-09-01
126,4e-30 g11170140/sp145659 PURATIVE BNDGUCANSE TYPE
KRECURSOR (EN
Seq primer: T3
High quality sequence stop: 289.
Location/Qualifiers
1..299
Location/Qualifiers
/organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="a3b03fs"
/clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XbaI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XbaI site of pBluescript"

FEATURES
source
1..299
Location/Qualifiers

BASE COUNT 65 a 84 c 54 g 96 t

Query Match 7.1%; Score 76.4; DB 13; Length 299;
Best Local Similarity 67.7%; Pred. No. 2.7e-09;
Matches 107; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy	449	GTGCTGCTCCGCTAATGATGAAACA	CTGCTACTGGGATTTGTGTAAGCTTCTTGCA	508
Db	142	GTGCTGCTTCTGGAAGTGGCCACTCTA	CTGATGGAAGCTGCAAGCCTTCTTGCT	201
Qy	509	GTGAGCCCGGTAAGGCTGATGTCA	CTCCCTGTTGGCTCCTGTAACAAGATGTAGA	568
Db	202	CTTGAGCGGCAAGGCTTAAGTCA	AGCGCCCTGCTGTGACTTGTGACACAAAGATAAC	261
Qy	569	CTCTTGCTGATTAACAACACTCA	AAACGGCTGTGTGT 606	
Db	262	CTATCACTAACCTGAAGCTGTCA	ACGCTGTGAGGGT 299	

Search completed: June 17, 2003, 18:49:27
Job time: 1462.69 secs

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